

(1) GENERAL INFORMATION:

- (i) APPLICANTS: Goodearl, Andrew; Stroobant, Paul; Minghetti, Luisa; Waterfield, Michael; Marchioni, Mark; Chen, Maio Su; Hiles, Ian
- (ii) TITLE OF INVENTION: Glial Mitogenic Factors, Their Preparation and Use
- (iii) NUMBER OF SEQUENCES: 184
- (iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Felfe & Lynch
(B) STREET: 805 Third Avenue
(C) CITY: New York City
(D) STATE: New York
(E) COUNTRY: USA
(F) ZIP: 10022
- (v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Diskette, 5.25 inch, 360 kb storage
(B) COMPUTER: IBM
(C) OPERATING SYSTEM: PC-DOS
(D) SOFTWARE: Wordperfect
- (vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:
- (vi) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 08/036,555
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- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/965,173
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- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/940,389
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- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/907,138
(B) FILING DATE: 30-JUN-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: 07/863,703
(B) FILING DATE: 03-APRIL-1992

(vii) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: U.K. 91 07566.3
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(viii) ATTORNEY/AGENT INFORMATION:

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- (C) REFERENCE/DOCKET NUMBER: LUD 5250.18

(ix) TELECOMMUNICATION INFORMATION:

- (A) TELEPHONE: (212) 688-9200
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

Phe Lys Gly Asp Ala His Thr Glu
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 3:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 10 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

Xaa Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 4:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

Xaa Lys Leu Gly Glu Met Trp Ala Glu
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 5:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Xaa Leu Gly Glu Lys Arg Ala
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 6:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

Xaa Ile Lys Ser Glu His Ala Gly Leu Ser Ile Gly Asp Thr Ala Lys
 1 5 10 15

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 7:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

Xaa Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 8:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

Xaa Ile Lys Gly Glu His Pro Gly Leu Ser Ile Gly Asp Val Ala Lys
 1 5 10 15

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 9:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine and Xaa in position 12 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9:

Xaa Met Ser Glu Tyr Ala Phe Phe Val Gln Thr Xaa Arg
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 10:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 14
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10:

Xaa Ser Glu His Pro Gly Leu Ser Ile Gly Asp Thr Ala Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 11:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine; Xaa in position 8 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11:

Xaa Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 12:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 7 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12:

Xaa Lys Leu Glu Phe Leu Xaa Ala Lys
1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 13:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13:

Xaa Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 14:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14:

Xaa Ala Lys Glu Ala Leu Ala Ala Leu Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 15:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 15:

Xaa Phe Val Leu Gln Ala Lys Lys
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 16:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 6
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 16:

Xaa Leu Gly Glu Met Trp
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 17:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 17:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
 1 5 10 15

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 18:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 10
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 8 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 18:

Glu Ala Lys Tyr Phe Ser Lys Xaa Asp Ala
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 19:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 7
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 2 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 19:

Glu Xaa Lys Phe Tyr Val Pro
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 20:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 26
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 20:

Glu Leu Ser Phe Ala Ser Val Arg Leu Pro Gly Cys Pro Pro Gly Val
 1 5 10 15

Asp Pro Met Val Ser Phe Pro Val Ala Leu
 20 25

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 21:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 2003
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: N in positions 31 and 32 could be either A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 21:

GGAATTCCTT	TTTTTTTTTT	TTTTTTTCTT	NNTTTTTTTTT	TGCCCTTATA	CCTCTTCGCC	60										
TTTCTGTGGT	TCCATCCACT	TCTTCCCCCT	CCTCCTCCCA	TAAACAACCTC	TCCTACCCCT	120										
GCACCCCCAA	TAAATAAATA	AAAGGAGGAG	GGCAAGGGGG	GAGGAGGAGG	AGTGGTGCTG	180										
CGAGGGGAAG	GAAAAGGGAG	GCAGCGCGAG	AAGAGCCGGG	CAGAGTCCGA	ACCGACAGCC	240										
AGAAGCCCGC	ACGCACCTCG	CACC	ATG	AGA	TGG	CGA	CGC	GCC	CCG	CGC	CGC	291				
		Met	Arg	Trp	Arg	Arg	Ala	Pro	Arg	Arg						
		1								5						
TCC	GGG	CGT	CCC	GGC	CCC	CGG	GCC	CAG	CGC	CCC	GGC	TCC	GCC	GCC	CGC	339
Ser	Gly	Arg	Pro	Gly	Pro	Arg	Ala	Gln	Arg	Pro	Gly	Ser	Ala	Ala	Arg	
10						15				20					25	
TCG	TCG	CCG	CCG	CTG	CCG	CTG	CTG	CCA	CTA	CTG	CTG	CTG	CTG	GGG	ACC	387
Ser	Ser	Pro	Pro	Leu	Pro	Leu	Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Thr	
				30					35					40		
GCG	GCC	CTG	GCG	CCG	GGG	GCG	GCG	GCC	GGC	AAC	GAG	GCG	GCT	CCC	GCG	435
Ala	Ala	Leu	Ala	Pro	Gly	Ala	Ala	Ala	Gly	Asn	Glu	Ala	Ala	Pro	Ala	
			45					50					55			
GGG	GCC	TCG	GTG	TGC	TAC	TCG	TCC	CCG	CCC	AGC	GTG	GGA	TCG	GTG	CAG	483
Gly	Ala	Ser	Val	Cys	Tyr	Ser	Ser	Pro	Pro	Ser	Val	Gly	Ser	Val	Gln	
		60					65					70				
GAG	CTA	GCT	CAG	CGC	GCC	GCG	GTG	GTG	ATC	GAG	GGA	AAG	GTG	CAC	CCG	531
Glu	Leu	Ala	Gln	Arg	Ala	Ala	Val	Val	Ile	Glu	Gly	Lys	Val	His	Pro	
	75					80					85					
CAG	CGG	CGG	CAG	CAG	GGG	GCA	CTC	GAC	AGG	AAG	GCG	GCG	GCG	GCG	GCG	579
Gln	Arg	Arg	Gln	Gln	Gly	Ala	Leu	Asp	Arg	Lys	Ala	Ala	Ala	Ala	Ala	
90					95					100					105	
GGC	GAG	GCA	GGG	GCG	TGG	GGC	GGC	GAT	CGC	GAG	CCG	CCA	GCC	GCG	GGC	627
Gly	Glu	Ala	Gly	Ala	Trp	Gly	Gly	Asp	Arg	Glu	Pro	Pro	Ala	Ala	Gly	
				110				115						120		
CCA	CGG	GCG	CTG	GGG	CCG	CCC	GCC	GAG	GAG	CCG	CTG	CTC	GCC	GCC	AAC	675
Pro	Arg	Ala	Leu	Gly	Pro	Pro	Ala	Glu	Glu	Pro	Leu	Leu	Ala	Ala	Asn	
			125					130					135			

GGG Gly	ACC Thr	GTG Val	CCC Pro	TCT Ser	TGG Trp	CCC Pro	ACC Thr	GCC Ala	CCG Pro	GTG Val	CCC Pro	AGC Ser	GCC Ala	GGC Gly	GAG Glu	723
		140					145					150				
CCC Pro	GGG Gly	GAG Glu	GAG Glu	GCG Ala	CCC Pro	TAT Tyr	CTG Leu	GTG Val	AAG Lys	GTG Val	CAC His	CAG Gln	GTG Val	TGG Trp	GCG Ala	771
	155					160					165					
GTG Val	AAA Lys	GCC Ala	GGG Gly	GGC Gly	TTG Leu	AAG Lys	AAG Lys	GAC Asp	TCG Ser	CTG Leu	CTC Leu	ACC Thr	GTG Val	CGC Arg	CTG Leu	819
	170				175					180					185	
GGG Gly	ACC Thr	TGG Trp	GGC Gly	CAC His	CCC Pro	GCC Ala	TTC Phe	CCC Pro	TCC Ser	TGC Cys	GGG Gly	AGG Arg	CTC Leu	AAG Lys	GAG Glu	867
				190					195					200		
GAC Asp	AGC Ser	AGG Arg	TAC Tyr	ATC Ile	TTC Phe	TTC Phe	ATG Met	GAG Glu	CCC Pro	GAC Asp	GCC Ala	AAC Asn	AGC Ser	ACC Thr	AGC Ser	915
			205					210					215			
CGC Arg	GCG Ala	CCG Pro	GCC Ala	GCC Ala	TTC Phe	CGA Arg	GCC Ala	TCT Ser	TTC Phe	CCC Pro	CCT Pro	CTG Leu	GAG Glu	ACG Thr	GGC Gly	963
		220					225					230				
CGG Arg	AAC Asn	CTC Leu	AAG Lys	AAG Lys	GAG Glu	GTC Val	AGC Ser	CGG Arg	GTG Val	CTG Leu	TGC Cys	AAG Lys	CGG Arg	TGC Cys	GCC Ala	1011
	235					240					245					
TTG Leu	CCT Pro	CCC Pro	CAA Gln	TTG Leu	AAA Lys	GAG Glu	ATG Met	AAA Lys	AGC Ser	CAG Gln	GAA Glu	TCG Ser	GCT Ala	GCA Ala	GGT Gly	1059
	250				255					260					265	
TCC Ser	AAA Lys	CTA Leu	GTC Val	CTT Leu	CGG Arg	TGT Cys	GAA Glu	ACC Thr	AGT Ser	TCT Ser	GAA Glu	TAC Tyr	TCC Ser	TCT Ser	CTC Leu	1107
				270					175					180		
AGA Arg	TTC Phe	AAG Lys	TGG Trp	TTC Phe	AAG Lys	AAT Asn	GGG Gly	AAT Asn	GAA Glu	TTG Leu	AAT Asn	CGA Arg	AAA Lys	AAC Asn	AAA Lys	1155
			185				190					195				
CCA Pro	CAA Gln	AAT Asn	ATC Ile	AAG Lys	ATA Ile	CAA Gln	AAA Lys	AAG Lys	CCA Pro	GGG Gly	AAG Lys	TCA Ser	GAA Glu	CTT Leu	CGC Arg	1203
		200					205					210				
ATT Ile	AAC Asn	AAA Lys	GCA Ala	TCA Ser	CTG Leu	GCT Ala	GAT Asp	TCT Ser	GGA Gly	GAG Glu	TAT Tyr	ATG Met	TGC Cys	AAA Lys	GTG Val	1251
	215					220					225					
ATC Ile	AGC Ser	AAA Lys	TTA Leu	GGA Gly	AAT Asn	GAC Asp	AGT Ser	GCC Ala	TCT Ser	GCC Ala	AAT Asn	ATC Ile	ACC Thr	ATC Ile	GTG Val	1299
	230				235					240					245	

GAA TCA AAC GCT ACA TCT ACA TCC ACC ACT GGG ACA AGC CAT CTT GTA	1347
Glu Ser Asn Ala Thr Ser Thr Ser Thr Thr Gly Thr Ser His Leu Val	
250 255 260	
AAA TGT GCG GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGG GAG TGC	1395
Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys	
265 270 275	
TTC ATG GTG AAA GAC CTT TCA AAC CCC TCG AGA TAC TTG TGC AAG TGC	1443
Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys	
280 285 290	
CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC	1491
Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser	
295 300 305	
TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA	1530
Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	
400 405 410	
TAGGAGCATG CTCAGTTGGT GCTGCTTTCT TGTTGCTGCA TCTCCCCTCA GATTCCACCT	1590
AGAGCTAGAT GTGTCTTACC AGATCTAATA TTGACTGCCT CTGCCTGTCTG CATGAGAACA	1650
TTAACAAAAG CAATTGTATT ACTTCCTCTG TTCGCGACTA GTTGGCTCTG AGATACTAAT	1710
AGGTGTGTGA GGCTCCGGAT GTTTCTGGAA TTGATATTGA ATGATGTGAT ACAAATTGAT	1770
AGTCAATATC AAGCAGTGAA ATATGATAAT AAAGGCATTT CAAAGTCTCA CTTTATTGA	1830
TAAAATAAAA ATCATTCTAC TGAACAGTCC ATCTTCTTTA TACAATGACC ACATCCTGAA	1890
AAGGGTGTG CTAAGCTGTA ACCGATATGC ACTTGAAATG ATGGTAAGTT AATTTTGATT	1950
CAGAATGTGT TATTTGTCAC AAATAAACAT AATAAAAGGA AAAAAAAAAA AAA	2003

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 22:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 11 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Xaa Lys
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 23:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 9 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 23:

Thr Glu Thr Ser Ser Ser Gly Leu Xaa Leu Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 24:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 24:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 25:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 9
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 7 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 25:

Ala Gly Tyr Phe Ala Glu Xaa Ala Arg
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 26:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 26:

Thr Thr Glu Met Ala Ser Glu Gln Gly Ala
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 27:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 27:

Ala Lys Glu Ala Leu Ala Ala Leu Lys
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 28:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 7
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 28:

Phe Val Leu Gln Ala Lys Lys
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 29:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 29:

Glu Thr Gln Pro Asp Pro Gly Gln Ile Leu Lys Lys Val Pro Met Val
1 5 10 15

Ile Gly Ala Tyr Thr
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 30:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in positions 1, 3, 17 and 19 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 30:

Xaa Glu Xaa Lys Glu Gly Arg Gly Lys Gly Lys Gly Lys Lys Glu
1 5 10 15

Xaa Gly Xaa Gly Lys
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 31:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 31:

Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 32:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 6 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 32:

Lys Leu Glu Phe Leu Xaa Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 33:

Xaa Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
Xaa in position 11 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 34:

Xaa Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 35:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine,
 Xaa in position 13 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 35:

Xaa Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 36:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 9
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 36:

Xaa Trp Phe Val Val Ile Glu Gly Lys
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 37:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 16
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 37:

Xaa Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 38:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 38:

Xaa Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 39:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 7
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 1 is Lysine or Arginine;
Xaa in position 6 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 39:

Xaa Asp Leu Leu Leu Xaa Val
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 40:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 39
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 40:

Cys Thr Cys Gly Cys Cys Lys Cys Cys Arg Thr Thr Cys Ala Cys Arg
1 5 10 15

Cys Ala Gly Ala Ala Gly Gly Thr Cys Thr Thr Cys Thr Cys Cys Thr
20 25 30

Thr Cys Thr Cys Ala Gly Cys
35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 41:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 24
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 41:

Cys Cys Thr Cys Gly Cys Thr Cys Cys Thr Thr Cys Thr Thr Cys Thr
1 5 10 15

Thr Gly Cys Cys Cys Thr Thr Cys
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 42:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 42:

AAGTGCCCAA ATGAGTTTAC TGGTGATCGC TGCCAAAACT ACGTAATGGC CAGCTTCTAC

60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 43:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 43:

AGTACGTCCA CTCCCTTTCT GTCTCTGCCT GAATAG

36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 44:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 569
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 44:

AAGGCGGAGG	AGCTGTACCA	GAAGAGAGTG	CTGACCATAA	CCGGCATCTG	CATCGCCCTC	60
CTTGTTGGTCG	GCATCATGTG	TGTGGTGGCC	TACTGCAAAA	CCAAGAAACA	GCGGAAAAAG	120
CTGCATGACC	GTCTTCGGCA	GAGCCTTCGG	TCTGAACGAA	ACAATATGAT	GAACATTGCC	180
AATGGGCCTC	ACCATCCTAA	CCCCCCCCC	GAGAATGTCC	AGCTGGTGAA	TCAATACGTA	240
TCTAAAAACG	TCATCTCCAG	TGAGCATATT	GTTGAGAGAG	AAGCAGAGAC	ATCCTTTTCC	300
ACCAGTCACT	ATACTTCCAC	AGCCCATCAC	TCCACTACTG	TCACCCAGAC	TCCTAGCCAC	360
AGCTGGAGCA	ACGGACACAC	TGAAAGCATC	CTTTCCGAAA	GCCACTCTGT	AATCGTGATG	420
TCATCCGTAG	AAAACAGTAG	GCACAGCAGC	CCAAGTGGGG	GCCCAAGAGG	ACGTCTTAAT	480
GGCACAGGAG	GCCCTCGTGA	ATGTAACAGC	TTCCTCAGGC	ATGCCAGAGA	AACCCCTGAT	540
TCCTACCGAG	ACTCTCCTCA	TAGTGAAAG				569

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 45:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 8
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 45:

Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 46:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in position 10 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 46:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 47:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 13
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 12 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 47:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 48:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 8
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 48:

Trp Phe Val Val Ile Glu Gly Lys
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 49:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 15
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 49:

Ala Ser Pro Val Ser Val Gly Ser Val Gln Glu Leu Val Gln Arg
 1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 50:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 50:

Val Cys Leu Leu Thr Val Ala Ala Leu Pro Pro Thr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 51:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 9
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 51:

Lys Val His Gln Val Trp Ala Ala Lys
1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 52:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 52:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 53:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 5 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 53:

Asp Leu Leu Leu Xaa Val
 1 5

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 54:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 54:

TTYAARGGNG AYGNCAYAC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 55:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 55:

CATRTAYTCR TAYTCRTCNG C 21

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 56:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 56:

TGYTCNGANG CCATYTCNGT 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 57:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 57:

TGYTCRCTNG CCATYTCNGT 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 58:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 58:

CCDATNACCA TNGGNACYTT 20

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 59:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 59:

GCNGCCCANA CYTGRTGNAC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 60:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 60:

GCYTCNGGYT CCATRAARAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 61:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 61:

CCYTCDATNA CNACRAACCA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 62:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 17
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 62:

TCNGCRAART ANCCNGC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 63:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 63:

GCNGCNAGNG CYTCYTNGC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 64:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 64:

GCNGCYAANG CYTCYTNGC 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 65:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 65:

TTYTTNGCYT GNAGNACRAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 66:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 66:

TTYTTNGCYT GYAANACRAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 67:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67:

TGNACNAGYT CYTGNAC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 68:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 68:

TGNACYAAYT CYTGNAC 17

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 69:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 69:

CATRTAYTCN CCNGARTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 70:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 70:

CATRTAYTCN CCRCTRTCNG C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 71:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 71:

NGARTCNGCY AANGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 72:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 72:

NGARTCNGCN AGNGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 73:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 73:

RCTRTCNGCY AANGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 74:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 74:

RCTRTCNGCN AGNGANGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 75:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 75:

NGARTCNGCY AARCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 76:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 76:

NGARTCNGCN AGRCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 77:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 77:

GTATGTGTCA	GCCATGACCA	CCCCGGCTCG	TATGTCACCT	GTAGATTTCC	ACACGCCAAG	60
CTCCCCCAA	TCGCCCCCTT	CGGAAATGTC	TCCACCCGTG	TCCAGCATGA	CGGTGTCCAT	120
GCCTTCCATG	GCGGTCAGCC	CCTTCATGGA	AGAAGAGAGA	CCTCTACTTC	TCGTGACACC	180
ACCAAGGCTG	CGGGAGAAGA	AGTTTGACCA	TCACCCTCAG	CAGTTCAGCT	CCTTCCACCA	240
CAACCCGCG	CATGACAGTA	ACAGCCTCCC	TGCTAGCCCC	TTGAGGATAG	TGGAGGATGA	300
GGAGTATGAA	ACGACCCAAG	AGTACGAGCC	AGCCCAAGAG	CCTGTTAAGA	AACTCGCCAA	360
TAGCCGGCGG	GCCAAAAGAA	CCAAGCCCAA	TGGCCACATT	GCTAACAGAT	TGGAAGTGGA	420
CAGCAACACA	AGCTCCCAGA	GCAGTAACTC	AGAGAGTGAA	ACAGAAGATG	AAAGAGTAGG	480
TGAAGATACG	CCTTTCCTGG	GCATACAGAA	CCCCCTGGCA	GCCAGTCTTG	AGGCAACACC	540
TGCCTTCCGC	CTGGCTGACA	GCAGGACTAA	CCCAGCAGGC	CGCTTCTCGA	CACAGGAAGA	600
AATCCAGGCC	AGGCTGTCTA	GTGTAATTGC	TAACCAAGAC	CCTATTGCTG	TATAAACCT	660
AAATAAACAC	ATAGATTAC	CTGTAAAACT	TTATTTTATA	TAATAAAGTA	TTCCACCTTA	720
AATTAAACAA						730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 78:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 78:

RCTRTCNGCY AARCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 79:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 79:

RCTRCTNGCN AGRCTNGCYT T 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 80:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 80:

ACNACNGARA TGGCTCNNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 81:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 81:

ACNACNGARA TGGCAGYNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 82:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 20
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 82:

CAYCARGTNT GGGCNGCNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 83:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 83:

TTYGTNGTNA THGARGGNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 84:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 84:

AARGGNGAYG CNCAYACNGA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 85:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 85:

GARGCNYTNG CNGCNYTNAA 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 86:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 86:

GTNGGNTCNG TNCARGARYT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 87:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 87:

GTNGGNAGYG TNCARGARYT 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 88:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 88:

NACYTTYTTN ARDATYTGNC C 21

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 89:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: Xaa in positions 14, 23, 90, 100, 126, and 135 is a stop codon.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 89:

TCTAA AAC TAC AGA GAC TGT ATT TTC ATG ATC ATC ATA GTT CTG TGA AAT ATA 53
Asn Tyr Arg Asp Cys Ile Phe Met Ile Ile Ile Val Leu Xaa Asn Ile
1 5 10 15

CTT AAA CCG CTT TGG TCC TGA TCT TGT AGG AAG TCA GAA CTT CGC ATT 101
Leu Lys Pro Leu Trp Ser Xaa Ser Cys Arg Lys Ser Glu Leu Arg Ile
20 25 30

AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC 149
Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Ser Met Cys Lys Val Ile
35 40 45

AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG	197
Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Arg Ile Val Glu	
50 55 60	
TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA	245
Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg	
65 70 75 80	
GGA GTG ATC AAG GTA TGT GGT CAC ACT TGA ATC ACG CAG GTG TGT GAA	293
Gly Val Ile Lys Val Cys Gly His Thr Xaa Ile Thr Gln Val Cys Glu	
85 90 95	
ATC TCA TTG TGA ACA AAT AAA AAT CAT GAA AGG AAA ACT CTA TGT TTG	341
Ile Ser Cys Xaa Thr Asn Lys Asn His Glu Arg Lys Thr Leu Cys Leu	
100 105 110	
AAA TAT CTT ATG GGT CCT CCT GTA AAG CTC TTC ACT CCA TAA GGT GAA	389
Lys Tyr Leu Met Gly Pro Pro Val Lys Leu Phe Thr Pro Xaa Gly Glu	
115 120 125	
ATA GAC CTG AAA TAT ATA TAG ATT ATT T	417
Ile Asp Leu Lys Tyr Ile Xaa Ile Ile	
130 135	

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 90:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 19, 25, and 31 is Inosine.
Y can be cytidine or thymidine.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 90:

CCGAATTCTG CAGGARACNC ARCCNGAYCC NGG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 91:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 14, 20, 23, 29, and 35 is Inosine.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 91:

AAGGATCCTG CAGNGTRTAN GCNCCDATNA CCATNGG

37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 92:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 16, 21, and 24 is Inosine. Y can be cytidine or thymidine.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 92:

CCGAATTCTG CAGGCNGAYT CNGGNGARTA YATG 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 93:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 33
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
 - (D) OTHER INFORMATION: N at positions 16 and 25 is Inosine. Y can be cytidine or thymidine.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 93:

CCGAATTCTG CAGGCNGAYA GYGGNGARTA YAT 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 94:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 14, 15, 16, 26, and 29 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 94:

AAGGATCCTG CAGNNNCATR TAYTCNCCNG ARTC 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 95:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 34
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 14, 15, 16, and 26 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 95:

AAGGATCCTG CAGNNNCATR TAYTCNCCRC TRTC 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 96:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 21, 28, and 31 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 96:

CCGAATTCTG CAGCAYCARG TNTGGGCNGC NAA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 97:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at position 31 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 97:

CCGAATTCTG CAGATHTTYT TYATGGARCC NGARG 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 98:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 35

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 18, 21, 24, 27, and 33 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 98:

CCGAATTCTG CAGGGGGNCC NCCNGCNTTY CCNGT 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 99:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 33

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: N at positions 21 and 24 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 99:

CCGAATTCTG CAGTGGTTYG TNGTNATHGA RGG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 100:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N at positions 17, 20, and 26 is Inosine.
 Y can be cytidine or thymidine.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 100:

AAGGATCCTG CAGYTTNGCU NGCCCANACY TGRTG 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 101:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N at position 19 is Inosine. Y can be
 cytidine or thymidine.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 101:

AAGGATCCTG CAGGCYTCNG GYTCCATRAA RAA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 102:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N at positions 16, 22, 25, 28, and 31 is
 Inosine.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 102:

AAGGATCCTG CAGACNGGRA ANGCNGGNGG NCC 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 103:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 35
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at positions 17, 26, and 29 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 103:

AAGGATCCTG CAGYTTNCCY TCDATNACNA CRAAC 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 104:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 18 is Inosine. Y can be
cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 104:

CATRTAYTCR TAYTCTCNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 19, 25, and 31 is Inosine.
Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 105:

CCGAATTCTG CAGAARGGNG AYGCNCAAYAC NGA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 106:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3 and 18 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 106:

GCNGCYAANG CYTCYTNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 107:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 33
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3, 6, 9, and 18 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 107:

GCNGCNAGNG CYTCYTNGC AAGGATCCTG CAG 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 30
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N at position 3, 12, and 15 is Inosine. Y can be cytidine or thymidine.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 108:

TCNGCRAART ANCCNGCAAG GATCCTGCAG 30

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 109:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 38
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 109:

CATCGATCTG CAGGCTGATT CTGGAGAATA TATGTGCA 38

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 110:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 110:

AAGGATCCTG CAGCCACATC TCGAGTCGAC ATCGATT 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 111:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 111:

CCGAATTCTG CAGTGATCAG CAAACTAGGA AATGACA 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 112:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 112:

CATCGATCTG CAGCCTAGTT TGCTGATCAC TTTGCAC 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 113:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 113:

AAGGATCCTG CAGTATATTC TCCAGAATCA GCCAGTG 37

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 114:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 34
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 114:

AAGGATCCTG CAGGCACGCA GTAGGCATCT CTTA 34

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 115:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 115:

CCGAATTCTG CAGCAGAACT TCGCATTAGC AAAGC 35

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 116:
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 116:

CATCCCGGGA TGAAGAGTCA GGAGTCTGTG GCA 33

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 117:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 117:

ATACCCGGGC TGCAGACAAT GAGATTTAC ACACCTGCG 39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 118:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 36
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 118:

AAGGATCCTG CAGTTTGGAA CCTGCCACAG ACTCCT 36

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 119:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 39
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 119:

ATACCCGGGC TGCAGATGAG ATTTACACA CCTGCGTGA 39

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 120:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 12
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 120:

His Gln Val Trp Ala Ala Lys Ala Ala Gly Leu Lys
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 121:

Gly Gly Leu Lys Lys Asp Ser Leu Leu Thr Val Arg Leu Gly Ala Asn
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 122:

Leu Gly Ala Trp Gly Pro Pro Ala Phe Pro Val Xaa Tyr
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 123:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 123:

Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser
1 5 10 15

Cys Gly Arg Leu Lys Glu Asp
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 124:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 13
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in position 10 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 124:

Tyr Ile Phe Phe Met Glu Pro Glu Ala Xaa Ser Ser Gly
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 125:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 23
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 125:

Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu Ala Asn Ser
 1 5 10 15

Ser Gly Gly Pro Gly Arg Leu
 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 126:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 14
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 126:

Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 127:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 127:

Glu Tyr Lys Cys Leu Lys Phe Lys Trp Phe Lys Lys Ala Thr Val Met
1 5 10 15

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 128:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 26
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 128:

Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys Trp Phe Lys
1 5 10 15

Asn Gly Ser Glu Leu Ser Arg Lys Asn Lys
20 25

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 129:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 13
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(ix) FEATURE:

(D) OTHER INFORMATION: Xaa in position 12 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 129:

Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Xaa Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 130:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 130:

Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met
1 5 10 15
Cys Lys Val Ile Ser Lys Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 12
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 131:

Ala Ser Leu Ala Asp Glu Tyr Glu Tyr Met Arg Lys
1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 132:

Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys
1 5 10 15
Lys Val Ile Ser Lys Leu
20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 744
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 133:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
	1				5				10						15		
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC		103
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
		20					25						30				
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG		151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu		
	35						40					45					
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
	50					55					60						
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG		247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val		
65					70				75						80		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG		295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
				85					90					95			
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA		343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
		100					105					110					
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
		115					120					125					
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys		
	130					135					140						
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		
145					150				155						160		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC		535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn		
				165					170					175			

ATC ACC ATT GTG GAG TCA AAC GGT AAG AGA TGC CTA CTG CGT GCT ATT	583
Ile Thr Ile Val Glu Ser Asn Gly Lys Arg Cys Leu Leu Arg Ala Ile	
180 185 190	
TCT CAG TCT CTA AGA GGA GTG ATC AAG GTA TGT GGT CAC ACT	625
Ser Gln Ser Leu Arg Gly Val Ile Lys Val Cys Gly His Thr	
195 200 205	
TGAATCACGC AGGTGTGTGA AATCTCATTG TGAACAAATA AAAATCATGA AAGGAAAAAA	685
AAAAAAAAAA AATCGATGTC GACTCGAGAT GTGGCTGCAG GTCGACTCTA GAGGATCCC	744

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 134:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1193
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 134:

CCTGCAG CAT CAA GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	55
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
1 5 10 15	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC	103
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
20 25 30	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	151
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
35 40 45	
GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	199
Ala Lys Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
50 55 60	
TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT GTG	247
Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala Val	
65 70 75 80	
CAA CGG TGC GCC TTG CCT CCC CGC TTG AAA GAG ATG AAG AGT CAG GAG	295
Gln Arg Cys Ala Leu Pro Pro Arg Leu Lys Glu Met Lys Ser Gln Glu	
85 90 95	
TCT GTG GCA GGT TCC AAA CTA GTG CTT CGG TGC GAG ACC AGT TCT GAA	343
Ser Val Ala Gly Ser Lys Leu Val Leu Arg Cys Glu Thr Ser Ser Glu	
100 105 110	

TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC	391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	
		115					120					125				
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG	439
Arg	Lys	Asn	Lys	Gly	Gly	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly	Lys	
	130					135					140					
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT	487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr	
	145				150					155					160	
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC	535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn	
			165						170					175		
ATC	ACC	ATT	GTG	GAG	TCA	AAC	GCC	ACA	TCC	ACA	TCT	ACA	GCT	GGG	ACA	583
Ile	Thr	Ile	Val	Glu	Ser	Asn	Ala	Thr	Ser	Thr	Ser	Thr	Ala	Gly	Thr	
			180					185					190			
AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	631
Ser	His	Leu	Val	Lys	Ser	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
		195					200					205				
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	679
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
	210					215					220					
TTG	TGC	AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	727
Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	
	225				230				235						240	
GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AGT	GCC	CAA	ATG	AGT	TTA	CTG	775
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Ser	Ala	Gln	Met	Ser	Leu	Leu	
			245					250						255		
GTG	ATC	GCT	GCC	AAA	ACT	ACG	TAATGGCCAG	CTTCTACAGT	ACGTCCACTC							826
Val	Ile	Ala	Ala	Lys	Thr	Thr										
			260													
CCTTTCTGTC	TCTGCCTGAA	TAGCGCATCT	CAGTCGGTGC	CGCTTTCTTG	TTGCCGCATC											886
TCCCCTCAGA	TTCCTCCTAG	AGCTAGATGC	GTTTTACCAG	GTCTAACATT	GA CTGCCTCT											946
GCCTGTGCGA	TGAGAACATT	AACACAAGCG	ATTGTATGAC	TTCCTCTGTC	CGTGACTAGT											1006
GGGCTCTGAG	CTACTCGTAG	GTGCGTAAGG	CTCCAGTGTT	TCTGAAATTG	ATCTTGAATT											1066
ACTGTGATAC	GACATGATAG	TCCCTCTCAC	CCAGTGCAAT	GACAATAAAG	GCCTTGAAAA											1126
GTCAAAAAAA	AAAAAATAAA	AAAAAATCGA	TGTCGACTCG	AGATGTGGCT	GCAGGTCGAC											1186
TCTAGAG																1193

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 135:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1108
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 135:

CCTGCAG	CAT	CAA	GTG	TGG	GCG	GCG	AAA	GCC	GGG	GGC	TTG	AAG	AAG	GAC	TCG	CTG	55
	His	Gln	Val	Trp	Ala	Ala	Lys	Ala	Gly	Gly	Leu	Lys	Lys	Asp	Ser	Leu	
1					5					10					15		
CTC	ACC	GTG	CGC	CTG	GGC	GCC	TGG	GGC	CAC	CCC	GCC	TTC	CCC	TCC	TGC		103
Leu	Thr	Val	Arg	Leu	Gly	Ala	Trp	Gly	His	Pro	Ala	Phe	Pro	Ser	Cys		
			20					25					30				
GGG	CGC	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	ATG	GAG	CCC	GAG		151
Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	Met	Glu	Pro	Glu		
			35				40					45					
GCC	AAC	AGC	AGC	GGC	GGG	CCC	GGC	CGC	CTT	CCG	AGC	CTC	CTT	CCC	CCC		199
Ala	Asn	Ser	Ser	Gly	Gly	Pro	Gly	Arg	Leu	Pro	Ser	Leu	Leu	Pro	Pro		
	50					55					60						
TCT	CGA	GAC	GGG	CCG	GAA	CCT	CAA	GAA	GGA	GGT	CAG	CCG	GGT	GCT	GTG		247
Ser	Arg	Asp	Gly	Pro	Glu	Pro	Gln	Glu	Gly	Gly	Gln	Pro	Gly	Ala	Val		
65					70					75					80		
CAA	CGG	TGC	GCC	TTG	CCT	CCC	CGC	TTG	AAA	GAG	ATG	AAG	AGT	CAG	GAG		295
Gln	Arg	Cys	Ala	Leu	Pro	Pro	Arg	Leu	Lys	Glu	Met	Lys	Ser	Gln	Glu		
				85					90					95			
TCT	GTG	GCA	GGT	TCC	AAA	CTA	GTG	CTT	CGG	TGC	GAG	ACC	AGT	TCT	GAA		343
Ser	Val	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu		
			100					105					110				
TAC	TCC	TCT	CTC	AAG	TTC	AAG	TGG	TTC	AAG	AAT	GGG	AGT	GAA	TTA	AGC		391
Tyr	Ser	Ser	Leu	Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser		
			115				120					125					
CGA	AAG	AAC	AAA	CCA	GAA	AAC	ATC	AAG	ATA	CAG	AAA	AGG	CCG	GGG	AAG		439
Arg	Lys	Asn	Lys	Pro	Glu	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Pro	Lys		
	130					135					140						
TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	GAA	TAT		487
Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly	Glu	Tyr		
145					150					155					160		
ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	GCC	AAC		535
Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	Ala	Asn		
				165					170					175			

ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG ACA	583
Ile Arg Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly Thr	
180 185 190	
AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	631
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
195 200 205	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	679
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
210 215 220	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	727
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
225 230 235 240	
GTA ATG GCC AGC TTC TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT	775
Val Met Ala Ser Phe Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro	
245 250 255	
GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG TTGCCGCATC TCCCCTCAGA TTCCGCCTAG	838
Glu	
AGCTAGATGC GTTTTACCAG GTCTAACATT GACTGCCTCT GCCTGTCGCA TGAGAACATT	898
AACACAAGCG ATTGTATGAC TTCCTCTGTC CGTGACTAGT GGGCTCTGAG CTA CTCTCGTAG	958
GTGCGTAAGG CTCCAGTGTT TCTGAAATTG ATCTTGAATT ACTGTGATAC GACATGATAG	1018
TCCCTCTCAC CCAGTGCAAT GACAATAAAG GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA	1078
AAAAATCGAT GTCGACTCGA GATGTGGCTG	1108

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 559
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (D) OTHER INFORMATION: N in position 214 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 136:

AGTTTCCCCC CCCAACTTGT CGGAACTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC	60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC	120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC	180
CCAGCGGCGC GCCAGCAGGA GCCACCCCGC GAGNCGTGCG ACCGGGACGG AGCGCCCGCC	240
AGTCCCAGGT GGCCCGGACC GCACGTTGCG TCCCCGCGCT CCCC GCCGGC GACAGGAGAC	300
GCTCCCCCCC ACGCCGCGCG CGCCTCGGCC CGGTCGCTGG CCCGCCTCCA CTCCGGGGAC	360
AAACTTTTCC CGAAGCCGAT CCCAGCCCTC GGACCCAAAC TTGTCGCGCG TCGCCTTCGC	420
CGGGAGCCGT CCGCGCAGAG CGTGCACTTC TCGGGCGAG ATG TCG GAG CGC AGA	474
Met Ser Glu Arg Arg	
1 5	

GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG	522
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly	
10 15 20	

AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA G	559
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala	
25 30	

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 137:
- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 252
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear
- (ix) FEATURE:
- (D) OTHER INFORMATION: N in position 8 could be either A or G.
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 137:

CC CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG	47
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser	
1 5 10 15	

CTG CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC	95
Leu Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser	
20 25 30	

TGC GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC	143
Cys Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro	
35 40 45	

GAG GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC	191
Glu Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro	
50 55 60	

CCC TCT CGA GAC GGG CCG GAA CCT CAA GAA GGA GGT CAG CCG GGT GCT	239
Pro Ser Arg Asp Gly Pro Glu Pro Gln Glu Gly Gly Gln Pro Gly Ala	
65 70 75	

GTG CAA CGG TGC G	252
Val Gln Arg Cys	
80	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 138:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 138:

CCT	TGC	CTC	CCC	GCT	TGA	AAG	AGA	TGA	AGA	GTC	AGG	AGT	CTG	TGG	CAG	48
Leu	Pro	Pro	Arg	Leu	Lys	Glu	His	Lys	Ser	Gln	Glu	Ser	Val	Ala	Gly	
1				5				10					15			
GTT	CCA	AAC	TAG	TGC	TTC	GGT	GCG	AGA	CCA	GTT	CTG	AAT	ACT	CCT	CTC	96
Ser	Lys	Leu	Val	Leu	Arg	Cys	Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	Leu	
			20				25					30				
TCA	AGT	TCA	AGT	GGT	TCA	AGA	ATG	GGA	GTG	AAT	TAA	GCC	GAA	AGA	ACA	144
Lys	Phe	Lys	Trp	Phe	Lys	Asn	Gly	Ser	Glu	Leu	Ser	Arg	Lys	Asn	Lys	
		35				40					45					
AAC	CAC	AAA	ACA	TCA	AGA	TAC	AGA	AAA	GGC	CGG	G					178
Pro	Gly	Asn	Ile	Lys	Ile	Gln	Lys	Arg	Pro	Gly						
	50					55										

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 139:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 139:

G	AAG	TCA	GAA	CTT	CGC	ATT	AGC	AAA	GCG	TCA	CTG	GCT	GAT	TCT	GGA	46
Lys	Ser	Glu	Leu	Arg	Ile	Ser	Lys	Ala	Ser	Leu	Ala	Asp	Ser	Gly		
1				5				10					15			
GAA	TAT	ATG	TGC	AAA	GTG	ATC	AGC	AAA	CTA	GGA	AAT	GAC	AGT	GCC	TCT	94
Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	Ser	Ala	Ser	
			20					25				30				
GCC	AAC	ATC	ACC	ATT	GTG	GAG	TCA	AAC	G							122
Ala	Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Ala							
			35													

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 140:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 417
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 140:

TCTAAACTA CAGAGACTGT ATTTTCATGA TCATCATAGT TCTGTGAAAT ATACTTAAAC	60
CGCTTTGGTC CTGATCTTGT AGG AAG TCA GAA CTT CGC ATT AGC AAA GCG	110
Lys Ser Glu Leu Arg Ile Ser Lys Ala	
1 5	
TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA CTA	158
Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys Leu	
10 15 20 25	
GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC GGT	206
Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn Gly	
30 35 40	
AAG AGA TGC CTA CTG CGT GCT ATT TCT CAG TCT CTA AGA GGA GTG ATC	254
Lys Arg Cys Leu Leu Arg Ala Ile Ser Gln Ser Leu Arg Gly Val Ile	
45 50 55	
AAG GTA TGT GGT CAC ACT TGAATCACGC AGGTGTGTGA AATCTCATTG	302
Lys Val Cys Gly His Thr	
60	
TGAACAAATA AAAATCATGA AAGGAAACT CTATGTTTGA AATATCTTAT GGGTCCTCCT	362
GTAAAGCTCT TCACTCCATA AGGTGAAATA GACCTGAAAT ATATATAGAT TATTT	417

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 141:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 141:

AG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT	47
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser	
1 5 10 15	
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT	95
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr	
20 25 30	
TCT TCA T	102
Ser Ser Ser	
35	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 142:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 142:

AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	GTG	CCC	48
Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	Val	Pro	
1				5				10						15		

ATG	AAA	GTC	CAA	ACC	CAA	GAA										69
Met	Lys	Val	Gln	Thr	Gln	Glu										
				20												

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 143:

AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	48
Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	
1				5				10						15		

GCC	AGC	TTC	TAC													60
Ala	Ser	Phe	Tyr													
				20												

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 144:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 36
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 144:

AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA	TAG					36
Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu						
1				5				10								

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 145:

AAG CAT CTT GGG ATT GAA TTT ATG GAG
Lys His Leu Gly Ile Glu Phe Met Glu
1 5

27

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 569

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 146:

AAA GCG GAG GAG CTC TAC CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT
Lys Ala Glu Glu Leu Tyr Gln Lys Arg Val Leu Thr Ile Thr Gly Ile
1 5 10 15

48

TGC ATC GCG CTG CTC GTG GTT GGC ATC ATG TGT GTG GTG GTC TAC TGC
Cys Ile Ala Leu Leu Val Val Gly Ile Met Cys Val Val Val Tyr Cys
20 25 30

96

AAA ACC AAG AAA CAA CGG AAA AAG CTT CAT GAC CGG CTT CGG CAG AGC
Lys Thr Lys Lys Gln Arg Lys Lys Leu His Asp Arg Leu Arg Gln Ser
35 40 45

144

CTT CGG TCT GAA AGA AAC ACC ATG ATG AAC GTA GCC AAC GGG CCC CAC
Leu Arg Ser Glu Arg Asn Thr Met Met Asn Val Ala Asn Gly Pro His
50 55 60

192

CAC CCC AAT CCG CCC CCC GAG AAC GTG CAG CTG GTG AAT CAA TAC GTA
His Pro Asn Pro Pro Pro Glu Asn Val Gln Leu Val Asn Gln Tyr Val
65 70 75 80

240

TCT AAA AAT GTC ATC TCT AGC GAG CAT ATT GTT GAG AGA GAG GCG GAG
Ser Lys Asn Val Ile Ser Ser Glu His Ile Val Glu Arg Glu Ala Glu
85 90 95

288

AGC TCT TTT TCC ACC AGT CAC TAC ACT TCG ACA GCT CAT CAT TCC ACT
Ser Ser Phe Ser Thr Ser His Tyr Thr Ser Thr Ala His His Ser Thr
100 105 110

336

ACT	GTC	ACT	CAG	ACT	CCC	AGT	CAC	AGC	TGG	AGC	AAT	GGA	CAC	ACT	GAA	384
Thr	Val	Thr	Gln	Thr	Pro	Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	
		115					120					125				
AGC	ATC	ATT	TCG	GAA	AGC	CAC	TCT	GTC	ATC	GTG	ATG	TCA	TCC	GTA	GAA	432
Ser	Ile	Ile	Ser	Glu	Ser	His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	
	130					135					140					
AAC	AGT	AGG	CAC	AGC	AGC	CCG	ACT	GGG	GGC	CCG	AGA	GGA	CGT	CTC	AAT	480
Asn	Ser	Arg	His	Ser	Ser	Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	
145					150					155					160	
GGC	TTG	GGA	GGC	CCT	CGT	GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	528
Gly	Leu	Gly	Gly	Pro	Arg	Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	
				165					170					175		
GAA	ACC	CCT	GAC	TCC	TAC	CGA	GAC	TCT	CCT	CAT	AGT	G	AAAG			569
Glu	Thr	Pro	Asp	Ser	Tyr	Arg	Asp	Ser	Pro	His	Ser					
		180						185								

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 730
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 147:

G	TAT	GTA	TCA	GCA	ATG	ACC	ACC	CCG	GCT	CGT	ATG	TCA	CCT	GTA	GAT	46
	Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	Arg	Met	Ser	Pro	Val	Asp	
1					5				10					15		
TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAG	TCA	CCC	CCT	TCG	GAA	ATG	TCC	CCG	94
Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	Pro	Ser	Glu	Met	Ser	Pro	
			20						25					30		
CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	TCC	ATG	GCG	GTC	AGT	CCC	142
Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	Ser	Met	Ala	Val	Ser	Pro	
			35					40					45			
TTC	GTG	GAA	GAG	GAG	AGA	CCC	CTG	CTC	CTT	GTG	ACG	CCA	CCA	CGG	CTG	190
Phe	Val	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	Val	Thr	Pro	Pro	Arg	Leu	
		50					55					60				
CGG	GAG	AAG	TAT	GAC	CAC	CAC	GCC	CAG	CAA	TTC	AAC	TCG	TTC	CAC	TGC	238
Arg	Glu	Lys	Tyr	Asp	His	His	Ala	Gln	Gln	Phe	Asn	Ser	Phe	His	Cys	
	65					70					75					

AAC CCC GCG CAT GAG AGC AAC AGC CTG CCC CCC AGC CCC TTG AGG ATA	286
Asn Pro Ala His Glu Ser Asn Ser Leu Pro Pro Ser Pro Leu Arg Ile	
80 85 90 95	
GTG GAG GAT GAG GAA TAT GAA ACG ACC CAG GAG TAC GAA CCA GCT CAA	334
Val Glu Asp Glu Glu Tyr Glu Thr Thr Gln Glu Tyr Glu Pro Ala Gln	
100 105 110	
GAG CCG GTT AAG AAA CTC ACC AAC AGC AGC CGG CGG GCC AAA AGA ACC	382
Glu Pro Val Lys Lys Leu Thr Asn Ser Ser Arg Arg Ala Lys Arg Thr	
115 120 125	
AAG CCC AAT GGT CAC ATT GCC CAC AGG TTG GAA ATG GAC AAC AAC ACA	430
Lys Pro Asn Gly His Ile Ala His Arg Leu Glu Met Asp Asn Asn Thr	
130 135 140	
GGC GCT GAC AGC AGT AAC TCA GAG AGC GAA ACA GAG GAT GAA AGA GTA	478
Gly Ala Asp Ser Ser Asn Ser Glu Ser Glu Thr Glu Asp Glu Arg Val	
145 150 155	
GGA GAA GAT ACG CCT TTC CTG GCC ATA CAG AAC CCC CTG GCA GCC AGT	526
Gly Glu Asp Thr Pro Phe Leu Ala Ile Gln Asn Pro Leu Ala Ala Ser	
160 165 170 175	
CTC GAG GCG GCC CCT GCC TTC CGC CTG GTC GAC AGC AGG ACT AAC CCA	574
Leu Glu Ala Ala Pro Ala Phe Arg Leu Val Asp Ser Arg Thr Asn Pro	
180 185 190	
ACA GGC GGC TTC TCT CCG CAG GAA GAA TTG CAG GCC AGG CTC TCC GGT	622
Thr Gly Gly Phe Ser Pro Gln Glu Glu Leu Gln Ala Arg Leu Ser Gly	
195 200 205	
GTA ATC GCT AAC CAA GAC CCT ATC GCT GTC TAAAACCGAA ATACACCCAT	672
Val Ile Ala Asn Gln Asp Pro Ile Ala Val	
210 215	
AGATTCACCT GTAAACTTT ATTTTATATA ATAAAGTATT CCACCTTAAA TTAAACAA	730

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 148:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1652
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 148:

AGTTTCCCCC CCCAACTTGT CGGAAGTCTG GGCTCGCGCG CAGGGCAGGA GCGGAGCGGC	60
GGCGGCTGCC CAGGCGATGC GAGCGCGGGC CGGACGGTAA TCGCCTCTCC CTCCTCGGGC	120
TGCGAGCGCG CCGGACCGAG GCAGCGACAG GAGCGGACCG CGGCGGGAAC CGAGGACTCC	180

CCAGCGGGCGC	GCCAGCAGGA	GCCACCCCGC	GAGCGTGCGA	CCGGGACGGA	GCGCCCGCCA	240
GTCCCAGGTG	GCCCGGACCG	CACGTTGCGT	CCCCGCGCTC	CCCGCCGGCG	ACAGGAGACG	300
CTCCCCCCCCA	CGCCGCGCGC	GCCTCGGCCC	GGTCGCTGGC	CCGCTCCAC	TCCGGGGACA	360
AACTTTTCCC	GAAGCCGATC	CCAGCCCTCG	GACCCAAACT	TGTCGCGCGT	CGCCTTCGCC	420
GGGAGCCGTC	CGCGCAGAGC	GTGCACTTCT	CGGGCGAG	ATG TCG GAG CGC AGA		473
				Met Ser Glu Arg Arg		
				1	5	
GAA GGC AAA GGC AAG GGG AAG GGC GGC AAG AAG GAC CGA GGC TCC GGG						521
Glu Gly Lys Gly Lys Gly Lys Gly Gly Lys Lys Asp Arg Gly Ser Gly						
	10			15	20	
AAG AAG CCC GTG CCC GCG GCT GGC GGC CCG AGC CCA GCC TTG CCT CCC						569
Lys Lys Pro Val Pro Ala Ala Gly Gly Pro Ser Pro Ala Leu Pro Pro						
	25			30	35	
CGC TTG AAA GAG ATG AAG ATG CAG GAG TCT GTG GCA GGT TCC AAA CTA						617
Arg Leu Lys Glu Met Lys Ser Gln Glu Ser Val Ala Gly Ser Lys Leu						
	40			45	50	
GTG CTT CGG TGC GAG ACC AGT TCT GAA TAC TCC TCT CTC AAG TTC AAG						665
Val Leu Arg Cys Glu Thr Ser Ser Glu Tyr Ser Ser Leu Lys Phe Lys						
	55			60	65	
TGG TTC AAG AAT GGG AGT GAA TTA AGC CGA AAG AAC AAA CCA CAA AAC						713
Trp Phe Lys Asn Gly Ser Gly Leu Ser Arg Lys Asn Lys Pro Gln Asn						
	70			75	80	85
ATC AAG ATA CAG AAA AGG CCG GGG AAG TCA GAA CTT CGC ATT AGC AAA						761
Ile Lys Ile Gln Lys Arg Pro Gly Lys Ser Glu Leu Arg Ile Ser Lys						
	90			95	100	
GCG TCA CTG GCT GAT TCT GGA GAA TAT ATG TGC AAA GTG ATC AGC AAA						809
Ala Ser Leu Ala Asp Ser Gly Glu Tyr Met Cys Lys Val Ile Ser Lys						
	105			110	115	
CTA GGA AAT GAC AGT GCC TCT GCC AAC ATC ACC ATT GTG GAG TCA AAC						857
Leu Gly Asn Asp Ser Ala Ser Ala Asn Ile Thr Ile Val Glu Ser Asn						
	120			125	130	
GAG ATC ACC ACT GGC ATG CCA GCC TCA ACT GAG ACA GCG TAT GTG TCT						905
Glu Ile Thr Thr Gly Met Pro Ala Ser Thr Glu Thr Ala Tyr Val Ser						
	135			140	145	
TCA GAG TCT CCC ATT AGA ATA TCA GTA TCA ACA GAA GGA ACA AAT ACT						953
Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Thr Asn Thr						
	150			155	160	165
TCT TCA TCC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG						1001
Ser Ser Ser Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys						
	170			175	180	

TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC	1049
Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe	
185 190 195	
ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG TGC AAG TGC CCA	1097
Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu Cys Lys Cys Pro	
200 205 210	
AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC GTA ATG GCC AGC TTC	1145
Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr Val Met Ala Ser Phe	
215 220 225	
TAC AGT ACG TCC ACT CCC TTT CTG TCT CTG CCT GAA TAGGCGCATG	1193
Tyr Ser Thr Ser Thr Pro Phe Leu Ser Leu Pro Glu	
230 235 240	
CTCAGTCGGT GCCGCTTTCT TGTTGCCGCA TCTCCCCTCA GATTCAACCT AGAGCTAGAT	1253
GCGTTTTACC AGGTCTAACA TTGACTGCCT CTGCCTGTCG CATGAGAACA TTAACACAAG	1313
CGATTGTATG ACTTCCTCTG TCCGTGACTA GTGGGCTCTG AGCTACTCGT AGGTGCGTAA	1373
GGCTCCAGTG TTTCTGAAAT TGATCTTGAA TTACTGTGAT ACGACATGAT AGTCCCTCTC	1433
ACCCAGTGCA ATGACAATAA AGGCCTTGAA AAGTCTCACT TTTATTGAGA AAATAAAAAAT	1493
CGTTCCACGG GACAGTCCCT CTTCTTTATA AAATGACCCT ATCCTTGAAA AGGAGGTGTG	1553
TTAAGTTGTA ACCAGTACAC ACTTGAAATG ATGGTAAGTT CGCTTCGGTT CAGAATGTGT	1613
TCTTTCTGAC AAATAAACAG AATAAAAAAA AAAAAAAAAA A	1652

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 149:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1140
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 149:

CAT CAN GTG TGG GCG GCG AAA GCC GGG GGC TTG AAG AAG GAC TCG CTG	48
His Gln Val Trp Ala Ala Lys Ala Gly Gly Leu Lys Lys Asp Ser Leu	
1 5 10 15	
CTC ACC GTG CGC CTG GGC GCC TGG GGC CAC CCC GCC TTC CCC TCC TGC	96
Leu Thr Val Arg Leu Gly Ala Trp Gly His Pro Ala Phe Pro Ser Cys	
20 25 30	
GGG CGC CTC AAG GAG GAC AGC AGG TAC ATC TTC TTC ATG GAG CCC GAG	144
Gly Arg Leu Lys Glu Asp Ser Arg Tyr Ile Phe Phe Met Glu Pro Glu	
35 40 45	
GCC AAC AGC AGC GGC GGG CCC GGC CGC CTT CCG AGC CTC CTT CCC CCC	192
Ala Asn Ser Ser Gly Gly Pro Gly Arg Leu Pro Ser Leu Leu Pro Pro	
50 55 60	

TCT Ser 65	CGA Arg	GAC Asp	GGG Gly	CCG Pro	GAA Glu 70	CCT Pro	CAA Gln	GAA Glu	GGA Gly	GGT Gly 75	CAG Gln	CCG Pro	GGT Gly	GCT Ala	GTG Val 80	240
CAA Gln	CGG Arg	TGC Cys	GCC Ala	TTG Leu 85	CCT Pro	CCC Pro	CGC Arg	TTG Leu	AAA Lys 90	GAG Glu	ATG Met	AAG Lys	AGT Ser	CAG Gln 95	GAG Glu	288
TCT Ser	GTG Val	GCA Ala	GGT Gly 100	TCC Ser	AAA Lys	CTA Leu	GTG Val	CTT Leu 105	CGG Arg	TGC Cys	GAG Glu	ACC Thr	AGT Ser 110	TCT Ser	GAA Glu	336
TAC Tyr	TCC Ser	TCT Ser 115	CTC Leu	AAG Lys	TTC Phe	AAG Lys	TGG Trp 120	TTC Phe	AAG Lys	AAT Asn	GGG Gly	AGT Ser 125	GAA Glu	TTA Leu	AGC Ser	384
CGA Arg 130	AAG Lys	AAC Asn	AAA Lys	CCA Pro	GAA Glu	AAC Asn 135	ATC Ile	AAG Lys	ATA Ile	CAG Gln	AAA Lys 140	AGG Arg	CCG Pro	GGG Gly	AAG Lys	432
TCA Ser 145	GAA Glu	CTT Leu	CGC Arg	ATT Ile	AGC Ser 150	AAA Lys	GCG Ala	TCA Ser	CTG Leu	GCT Ala 155	GAT Asp	TCT Ser	GGA Gly	GAA Glu	TAT Tyr 160	480
ATG Met	TGC Cys	AAA Lys	GTG Val	ATC Ile 165	AGC Ser	AAA Lys	CTA Leu	GGA Gly	AAT Asn 170	GAC Asp	AGT Ser	GCC Ala	TCT Ser	GCC Ala 175	AAC Asn	528
ATC Ile	ACC Thr	ATT Ile	GTG Val 180	GAG Glu	TCA Ser	AAC Asn	GCC Ala	ACA Thr 185	TCC Ser	ACA Thr	TCT Ser	ACA Thr	GCT Ala 190	GGG Gly	ACA Thr	576
AGC Ser	CAT His	CTT Leu 195	GTC Val	AAG Lys	TGT Cys	GCA Ala	GAG Glu 200	AAG Lys	GAG Glu	AAA Lys	ACT Thr 205	TTC Phe	TGT Cys	GTG Val	AAT Asn	624
GGA Gly 210	GGC Gly	GAG Glu	TGC Cys	TTC Phe	ATG Met	GTG Val 215	AAA Lys	GAC Asp	CTT Leu	TCA Ser	AAT Asn 220	CCC Pro	TCA Ser	AGA Arg	TAC Tyr	672
TTG Leu 225	TGC Cys	AAG Lys	TGC Cys	CAA Gln	CCT Pro 230	GGA Gly	TTC Phe	ACT Thr	GGA Gly	GCG Ala 235	AGA Arg	TGT Cys	ACT Thr	GAG Glu	AAT Asn 240	720
GTG Val	CCC Pro	ATG Met	AAA Lys	GTC Val 245	CAA Gln	ACC Thr	CAA Gln	GAA Glu	AAG Lys 250	TGC Cys	CCA Pro	AAT Asn	GAG Glu	TTT Phe 255	ACT Thr	768
GGT Gly	GAT Asp	CGC Arg	TGC Cys 260	CAA Gln	AAC Asn	TAC Tyr	GTA Val	ATG Met 265	GCC Ala	AGC Ser	TTC Phe	TAC Tyr	AGT Ser 270	ACG Thr	TCC Ser	816

ACT CCC TTT CTG TCT CTG CCT GAA TAGCGCATCT CAGTCGGTGC CGCTTTCTTG	870
Thr Pro Phe Leu Ser Leu Pro Glu	
275 280	

TTGCCGCAATC TCCCCTCAGA TTCCNCCTAG AGCTAGATGC GTTTTACCAG GTCTAACATT	930
GACTGCCTCT GCCTGTCGCA TGAGAACATT AACACAAGCG ATTGTATGAC TTCCTCTGTC	990
CGTGACTAGT GGGCTCTGAG CTACTCGTAG GTGCGTAAGG CTCCAGTGTT TCTGAAATTG	1050
ATCTTGAATT ACTGTGATAC GACATGATAG TCCCTCTCAC CCAGTGCAAT GACAATAAAG	1110
GCCTTGAAAA GTCAAAAAAA AAAAAAAAAA	1140

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 150:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1764
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 150:

G AAG TCA GAA CTT CGC ATT AGC AAA GCG TCA CTG GCT GAT TCT GGA GAA	49
Lys Ser Glu Leu Arg Ile Ser Lys Ala Ser Leu Ala Asp Ser Gly Glu	
1 5 10 15	

TAT ATG TGC AAA GTG ATC AGC AAA CTA GGA AAT GAC AGT GCC TCT GCC	97
Tyr Met Cys Lys Val Ile Ser Lys Leu Gly Asn Asp Ser Ala Ser Ala	
20 25 30	

AAC ATC ACC ATT GTG GAG TCA AAC GCC ACA TCC ACA TCT ACA GCT GGG	145
Asn Ile Thr Ile Val Glu Ser Asn Ala Thr Ser Thr Ser Thr Ala Gly	
35 40 45	

ACA AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG	193
Thr Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val	
50 55 60	

AAT GGA GGC GAC TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA	241
Asn Gly Gly Asp Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg	
65 70 75 80	

TAC TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG	289
Tyr Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu	
85 90 95	

AAT GTG CCC ATG AAA GTC CAA ACC CAA GAA AAA GCG GAG GAG CTC TAC	337
Asn Val Pro Met Lys Val Gln Thr Gln Glu Lys Ala Glu Glu Leu Tyr	
100 105 110	

CAG AAG AGA GTG CTC ACC ATT ACC GGC ATT TGC ATC GCG CTG CTC GTG	385
Gln Lys Arg Val Leu Thr Ile Thr Gly Ile Cys Ile Ala Leu Leu Val	
115 120 125	

GTT	GGC	ATC	ATG	TGT	GTG	GTG	GTC	TAC	TGC	AAA	ACC	AAG	AAA	CAA	CGG	433
Val	Gly	Ile	Met	Cys	Val	Val	Val	Tyr	Cys	Lys	Thr	Lys	Lys	Gln	Arg	
130						135					140					
AAA	AAG	CTT	CAT	GAC	CGG	CTT	CGG	CAG	AGC	CTT	CGG	TCT	GAA	AGA	AAC	481
Lys	Lys	Leu	His	Asp	Arg	Leu	Arg	Gln	Ser	Leu	Arg	Ser	Glu	Arg	Asn	
145					150					155					160	
ACC	ATG	ATG	AAC	GTA	GCC	AAC	GGG	CCC	CAC	CAC	CCC	AAT	CCG	CCC	CCC	529
Thr	Met	Met	Asn	Val	Ala	Asn	Gly	Pro	His	His	Pro	Asn	Pro	Pro	Pro	
				165					170					175		
GAG	AAC	GTG	CAG	CTG	GTG	AAT	CAA	TAC	GTA	TCT	AAA	AAT	GTC	ATC	TCT	577
Glu	Asn	Val	Gln	Leu	Val	Asn	Gln	Tyr	Val	Ser	Lys	Asn	Val	Ile	Ser	
			180					185					190			
AGC	GAG	CAT	ATT	GTT	GAG	AGA	GAG	GCG	GAG	AGC	TCT	TTT	TCC	ACC	AGT	625
Ser	Glu	His	Ile	Val	Glu	Arg	Glu	Ala	Glu	Ser	Ser	Phe	Ser	Thr	Ser	
		195					200					205				
CAC	TAC	ACT	TCG	ACA	GCT	CAT	CAT	TCC	ACT	ACT	GTC	ACT	CAG	ACT	CCC	673
His	Tyr	Thr	Ser	Thr	Ala	His	His	Ser	Thr	Thr	Val	Thr	Gln	Thr	Pro	
	210					215					220					
AGT	CAC	AGC	TGG	AGC	AAT	GGA	CAC	ACT	GAA	AGC	ATC	ATT	TCG	GAA	AGC	721
Ser	His	Ser	Trp	Ser	Asn	Gly	His	Thr	Glu	Ser	Ile	Ile	Ser	Glu	Ser	
225					230					235					240	
CAC	TCT	GTC	ATC	GTG	ATG	TCA	TCC	GTA	GAA	AAC	AGT	AGG	CAC	AGC	AGC	769
His	Ser	Val	Ile	Val	Met	Ser	Ser	Val	Glu	Asn	Ser	Arg	His	Ser	Ser	
				245					250					255		
CCG	ACT	GGG	GGC	CCG	AGA	GGA	CGT	CTC	AAT	GGC	TTG	GGA	GGC	CCT	CGT	817
Pro	Thr	Gly	Gly	Pro	Arg	Gly	Arg	Leu	Asn	Gly	Leu	Gly	Gly	Pro	Arg	
			260					265					270			
GAA	TGT	AAC	AGC	TTC	CTC	AGG	CAT	GCC	AGA	GAA	ACC	CCT	GAC	TCC	TAC	865
Glu	Cys	Asn	Ser	Phe	Leu	Arg	His	Ala	Arg	Glu	Thr	Pro	Asp	Ser	Tyr	
		275					280					285				
CGA	GAC	TCT	CCT	CAT	AGT	GAA	AGA	CAT	AAC	CTT	ATA	GCT	GAG	CTA	AGG	913
Arg	Asp	Ser	Pro	His	Ser	Glu	Arg	His	Asn	Leu	Ile	Ala	Glu	Leu	Arg	
	290					295					300					
AGA	AAC	AAG	GCC	CAC	AGA	TCC	AAA	TGC	ATG	CAG	ATC	CAG	CTT	TCC	GCA	961
Arg	Asn	Lys	Ala	His	Arg	Ser	Lys	Cys	Met	Gln	Ile	Gln	Leu	Ser	Ala	
305					310					315					320	
ACT	CAT	CTT	AGA	GCT	TCT	TCC	ATT	CCC	CAT	TGG	GCT	TCA	TTC	TCT	AAG	1009
Thr	His	Leu	Arg	Ala	Ser	Ser	Ile	Pro	His	Trp	Ala	Ser	Phe	Ser	Lys	
				325					330					335		

ACC	CCT	TGG	CCT	TTA	GGA	AGG	TAT	GTA	TCA	GCA	ATG	ACC	ACC	CCG	GCT	1057
Thr	Pro	Trp	Pro	Leu	Gly	Arg	Tyr	Val	Ser	Ala	Met	Thr	Thr	Pro	Ala	
			340					345					350			
CGT	ATG	TCA	CCT	GTA	GAT	TTC	CAC	ACG	CCA	AGC	TCC	CCC	AAG	TCA	CCC	1105
Arg	Met	Ser	Pro	Val	Asp	Phe	His	Thr	Pro	Ser	Ser	Pro	Lys	Ser	Pro	
		355					360					365				
CCT	TCG	GAA	ATG	TCC	CCG	CCC	GTG	TCC	AGC	ACG	ACG	GTC	TCC	ATG	CCC	1153
Pro	Ser	Glu	Met	Ser	Pro	Pro	Val	Ser	Ser	Thr	Thr	Val	Ser	Met	Pro	
	370					375					380					
TCC	ATG	GCG	GTC	AGT	CCC	TTC	GTG	GAA	GAG	GAG	AGA	CCC	CTG	CTC	CTT	1201
Ser	Met	Ala	Val	Ser	Pro	Phe	Val	Glu	Glu	Glu	Arg	Pro	Leu	Leu	Leu	
385					390					395					400	
GTG	ACG	CCA	CCA	CGG	CTG	CGG	GAG	AAG	TAT	GAC	CAC	CAC	GCC	CAG	CAA	1249
Val	Thr	Pro	Pro	Arg	Leu	Arg	Glu	Lys	Tyr	Asp	His	His	Ala	Gln	Gln	
				405					410					415		
TTC	AAC	TCG	TTC	CAC	TGC	AAC	CCC	GCG	CAT	GAG	AGC	AAC	AGC	CTG	CCC	1297
Phe	Asn	Ser	Phe	His	Cys	Asn	Pro	Ala	His	Glu	Ser	Asn	Ser	Leu	Pro	
			420					425					430			
CCC	AGC	CCC	TTG	AGG	ATA	GTG	GAG	GAT	GAG	GAA	TAT	GAA	ACG	ACC	CAG	1345
Pro	Ser	Pro	Leu	Arg	Ile	Val	Glu	Asp	Glu	Glu	Tyr	Glu	Thr	Thr	Gln	
		435				440						445				
GAG	TAC	GAA	CCA	GCT	CAA	GAG	CCG	GTT	AAG	AAA	CTC	ACC	AAC	AGC	AGC	1393
Glu	Tyr	Glu	Pro	Ala	Gln	Glu	Pro	Val	Lys	Lys	Leu	Thr	Asn	Ser	Ser	
	450					455					460					
CGG	CGG	GCC	AAA	AGA	ACC	AAG	CCC	AAT	GGT	CAC	ATT	GCC	CAC	AGG	TTG	1441
Arg	Arg	Ala	Lys	Arg	Thr	Lys	Pro	Asn	Gly	His	Ile	Ala	His	Arg	Leu	
465					470					475					480	
GAA	ATG	GAC	AAC	AAC	ACA	GGC	GCT	GAC	AGC	AGT	AAC	TCA	GAG	AGC	GAA	1489
Glu	Met	Asp	Asn	Asn	Thr	Gly	Ala	Asp	Ser	Ser	Asn	Ser	Glu	Ser	Glu	
				485					490					495		
ACA	GAG	GAT	GAA	AGA	GTA	GGA	GAA	GAT	ACG	CCT	TTC	CTG	GCC	ATA	CAG	1537
Thr	Glu	Asp	Glu	Arg	Val	Gly	Glu	Asp	Thr	Pro	Phe	Leu	Ala	Ile	Gln	
			500					505					510			
AAC	CCC	CTG	GCA	GCC	AGT	CTC	GAG	GCG	GCC	CCT	GCC	TTC	CGC	CTG	GTC	1585
Asn	Pro	Leu	Ala	Ala	Ser	Leu	Glu	Ala	Ala	Pro	Ala	Phe	Arg	Leu	Val	
		515					520					525				
GAC	AGC	AGG	ACT	AAC	CCA	ACA	GGC	GGC	TTC	TCT	CCG	CAG	GAA	GAA	TTG	1633
Asp	Ser	Arg	Thr	Asn	Pro	Thr	Gly	Gly	Phe	Ser	Pro	Gln	Glu	Glu	Leu	
	530					535					540					

CAG	GCC	AGG	CTC	TCC	GGT	GTA	ATC	GCT	AAC	CAA	GAC	CCT	ATC	GCT	GTC	1681
Gln	Ala	Arg	Leu	Ser	Gly	Val	Ile	Ala	Asn	Gln	Asp	Pro	Ile	Ala	Val	
545					550				555						560	

TAAAACCGAA	ATACACCCAT	AGATTCACCT	GTAAAACTTT	ATTTTATATA	ATAAAGTATT	1741
CCACCTTAAA	TAAACAAAA	AAA				1764

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 151:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 151:

Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	
1				5					10					15		
Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	
			20					25					30			
Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	
		35					40					45				
Phe	Tyr															
	50															

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 152:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 50
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 152:

Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	
1				5					10					15		
Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	
			20					25					30			
Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	Val	Pro	Met	Lys	
		35					40					45				
Val	Gln															
	50															

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 153:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 46
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 153:

Glu	Cys	Leu	Arg	Lys	Tyr	Lys	Asp	Phe	Cys	Ile	His	Gly	Glu	Cys	Lys	
1				5					10					15		
Tyr	Val	Lys	Glu	Leu	Arg	Ala	Pro	Ser	Cys	Lys	Cys	Gln	Gln	Glu	Tyr	
			20					25					30			
Phe	Gly	Glu	Arg	Cys	Gly	Glu	Lys	Ser	Asn	Lys	Thr	His	Ser			
		35					40					45				

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 154:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 198
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 154:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	144
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	
		35					40					45				
GTA	ATG	GCC	AGC	TTC	TAC	AGT	ACG	TCC	ACT	CCC	TTT	CTG	TCT	CTG	CCT	192
Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	Phe	Leu	Ser	Leu	Pro	
	50					55					60					
GAA	TAG															198
Glu																
65																

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 192
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 155:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	144
Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	
			35				40					45				
GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAA	GCG	GAG	GAG	CTC	TAC	TAA	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Ala	Glu	Glu	Leu	Tyr		
	50					55					60					

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 156:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CCA	AAT	GAG	TTT	ACT	GGT	GAT	CGC	TGC	CAA	AAC	TAC	144
Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	Arg	Cys	Gln	Asn	Tyr	
			35				40					45				
GTA	ATG	GCC	AGC	TTC	TAC	AAA	GCG	GAG	GAG	CTC	TAC	TAA				183
Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	Glu	Leu	Tyr					
	50					55					60					

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 157:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
1 5 10 15	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
20 25 30	
TTG TGC AAG TGC CCA AAT GAG TTT ACT GGT GAT CGC TGC CAA AAC TAC	144
Leu Cys Lys Cys Pro Asn Glu Phe Thr Gly Asp Arg Cys Gln Asn Tyr	
35 40 45	
GTA ATG GCC AGC TTC TAC AAG CAT CTT GGG ATT GAA TTT ATG GAG AAA	192
Val Met Ala Ser Phe Tyr Lys His Leu Gly Ile Glu Phe Met Glu Lys	
50 55 60	
GCG GAG GAG CTC TAC TAA	210
Ala Glu Glu Leu Tyr	
65	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 158:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 267
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 158:

AGC CAT CTT GTC AAG TGT GCA GAG AAG GAG AAA ACT TTC TGT GTG AAT	48
Ser His Leu Val Lys Cys Ala Glu Lys Glu Lys Thr Phe Cys Val Asn	
1 5 10 15	
GGA GGC GAG TGC TTC ATG GTG AAA GAC CTT TCA AAT CCC TCA AGA TAC	96
Gly Gly Glu Cys Phe Met Val Lys Asp Leu Ser Asn Pro Ser Arg Tyr	
20 25 30	
TTG TGC AAG TGC CAA CCT GGA TTC ACT GGA GCG AGA TGT ACT GAG AAT	144
Leu Cys Lys Cys Gln Pro Gly Phe Thr Gly Ala Arg Cys Thr Glu Asn	
35 40 45	

GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAG	TGC	CCA	AAT	GAG	TTT	ACT	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Cys	Pro	Asn	Glu	Phe	Thr	
50						55					60					
GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	TAC	AGT	ACG	TCC	240
Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	
65					70					75					80	
ACT	CCC	TTT	CTG	TCT	CTG	CCT	GAA	TAG								267
Thr	Pro	Phe	Leu	Ser	Leu	Pro	Glu									
					85											

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 159:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 252
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 159:

AGC	CAT	CTT	GTC	AAG	TGT	GCA	GAG	AAG	GAG	AAA	ACT	TTC	TGT	GTG	AAT	48
Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	Thr	Phe	Cys	Val	Asn	
1				5					10					15		
GGA	GGC	GAG	TGC	TTC	ATG	GTG	AAA	GAC	CTT	TCA	AAT	CCC	TCA	AGA	TAC	96
Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	Asn	Pro	Ser	Arg	Tyr	
			20					25					30			
TTG	TGC	AAG	TGC	CAA	CCT	GGA	TTC	ACT	GGA	GCG	AGA	TGT	ACT	GAG	AAT	144
Leu	Cys	Lys	Cys	Gln	Pro	Gly	Phe	Thr	Gly	Ala	Arg	Cys	Thr	Glu	Asn	
		35					40					45				
GTG	CCC	ATG	AAA	GTC	CAA	ACC	CAA	GAA	AAG	TGC	CCA	AAT	GAG	TTT	ACT	192
Val	Pro	Met	Lys	Val	Gln	Thr	Gln	Glu	Lys	Cys	Pro	Asn	Glu	Phe	Thr	
50						55					60					
GGT	GAT	CGC	TGC	CAA	AAC	TAC	GTA	ATG	GCC	AGC	TTC	TAC	AAA	GCG	GAG	240
Gly	Asp	Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	Tyr	Lys	Ala	Glu	
65					70					75					80	
GAG	CTC	TAC	TAA													252
Glu	Leu	Tyr														

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 160:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 160:

CC ACA TCC ACA TCT ACA GCT GGG ACA AGC CAT CTT GTC AAG TGT GCA	47
Thr Ser Thr Ser Thr Ala Gly Thr Ser His Leu Val Lys Cys Ala	
1 5 10 15	

GAG AAG GAG AAA ACT TTC TGT GTG AAT GGA GGC GAG TGC TTC ATG GTG	95
Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Cys Phe Met Val	
20 25 30	

AAA GAC CTT TCA AAT CCC TCA AGA TAC TTG T GC	128
Lys Asp Leu Ser Asn Pro Ser Arg Tyr Leu	
35 40	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 161:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 161:

A CAT AAC CTT ATA GCT GAG CTA AGG AGA AAC AAG GCC CAC AGA TCC	46
His Asn Leu Ile Ala Glu Leu Arg Arg Asn Lys Ala His Arg Ser	
1 5 10 15	

AAA TGC ATG CAG ATC CAG CTT TCC GCA ACT CAT CTT AGA GCT TCT TCC	94
Lys Cys Met Gln Ile Gln Leu Ser Ala Thr His Leu Arg Ala Ser Ser	
20 25 30	

ATT CCC CAT TGG GCT TCA TTC TCT AAG ACC CCT TGG CCT TTA GGA AG	141
Ile Pro His Trp Ala Ser Phe Ser Lys Thr Pro Trp Pro Leu Gly Arg	
35 40 45	

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 162:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 24
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: Xaa in positions 15 and 22 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 162:

Ala Ala Glu Lys Glu Lys Thr Phe Cys Val Asn Gly Gly Glu Xaa Phe
 1 5 10 15
 Met Val Lys Asp Leu Xaa Asn Pro
 20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 163:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 745
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 163:

ATG AGA TGG CGA CGC GCC CCG CGC CGC TCC GGG CGT CCC GGC CCC CGG	48
Met Arg Trp Arg Arg Ala Pro Arg Arg Ser Gly Arg Pro Gly Pro Arg	
1 5 10 15	
GCC CAG CGC CCC GGC TCC GCC GCC CGC TCG TCG CCG CCG CTG CCG CTG	96
Ala Gln Arg Pro Gly Ser Ala Ala Arg Ser Ser Pro Pro Leu Pro Leu	
20 25 30	
CTG CCA CTA CTG CTG CTG CTG GGG ACC GCG GCC CTG GCG CCG GGG GCG	144
Leu Pro Leu Leu Leu Leu Leu Gly Thr Ala Ala Leu Ala Pro Gly Ala	
35 40 45	
GCG GCC GGC AAC GAG GCG GCT CCC GCG GGG GCC TCG GTG TGC TAC TCG	192
Ala Ala Gly Asn Glu Ala Ala Pro Ala Gly Ala Ser Val Cys Tyr Ser	
50 55 60	
TCC CCG CCC AGC GTG GGA TCG GTG CAG GAG CTA GCT CAG CGC GCC GCG	240
Ser Pro Pro Ser Val Gly Ser Val Gln Glu Leu Ala Gln Arg Ala Ala	
65 70 75 80	
GTG GTG ATC GAG GGA AAG GTG CAC CCG CAG CGG CGG CAG CAG GGG GCA	288
Val Val Ile Glu Gly Lys Val His Pro Gln Arg Arg Gln Gln Gly Ala	
85 90 95	

CTC	GAC	AGG	AAG	GCG	GCG	GCG	GCG	GCG	GGC	GAG	GCA	GGG	GCG	TGG	GGC	336
Leu	Asp	Arg	Lys	Ala	Ala	Ala	Ala	Ala	Gly	Glu	Ala	Gly	Ala	Trp	Gly	
			100						105					110		
GGC	GAT	CGC	GAG	CCG	CCA	GCC	GCG	GGC	CCA	CGG	GCG	CTG	GGG	CCG	CCC	384
Gly	Asp	Arg	Glu	Pro	Pro	Ala	Ala	Gly	Pro	Arg	Ala	Leu	Gly	Pro	Pro	
			115						120					125		
GCC	GAG	GAG	CCG	CTG	CTC	GCC	GCC	AAC	GGG	ACC	GTG	CCC	TCT	TGG	CCC	432
Ala	Glu	Glu	Pro	Leu	Leu	Ala	Ala	Asn	Gly	Thr	Val	Pro	Ser	Trp	Pro	
			130						135					140		
ACC	GCC	CCG	GTG	CCC	AGC	GCC	GGC	GAG	CCC	GGG	GAG	GAG	GCG	CCC	TAT	480
Thr	Ala	Pro	Val	Pro	Ser	Ala	Gly	Glu	Pro	Gly	Glu	Glu	Ala	Pro	Tyr	
			145						150					155		160
CTG	GTG	AAG	GTG	CAC	CAG	GTG	TGG	GCG	GTG	AAA	GCC	GGG	GGC	TTG	AAG	528
Leu	Val	Lys	Val	His	Gln	Val	Trp	Ala	Val	Lys	Ala	Gly	Gly	Leu	Lys	
				165					170					175		
AAG	GAC	TCG	CTG	CTC	ACC	GTG	CGC	CTG	GGG	ACC	TGG	GGC	CAC	CCC	GCC	576
Lys	Asp	Ser	Leu	Leu	Thr	Val	Arg	Leu	Gly	Thr	Trp	Gly	His	Pro	Ala	
			180						185					190		
TTC	CCC	TCC	TGC	GGG	AGG	CTC	AAG	GAG	GAC	AGC	AGG	TAC	ATC	TTC	TTC	624
Phe	Pro	Ser	Cys	Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	
			195						200					205		
ATG	GAG	CCC	GAC	GCC	AAC	AGC	ACC	AGC	CGC	GCG	CCG	GCC	GCC	TTC	CGA	672
Met	Glu	Pro	Asp	Ala	Asn	Ser	Thr	Ser	Arg	Ala	Pro	Ala	Ala	Phe	Arg	
			210						215					220		
GCC	TCT	TTC	CCC	CCT	CTG	GAG	ACG	GGC	CGG	AAC	CTC	AAG	AAG	GAG	GTC	720
Ala	Ser	Phe	Pro	Pro	Leu	Glu	Thr	Gly	Arg	Asn	Leu	Lys	Lys	Glu	Val	
			225						230					235		240
AGC	CGG	GTG	CTG	TGC	AAG	CGG	TGC	G								745
Ser	Arg	Val	Leu	Cys	Lys	Arg	Cys									
				245												

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 164:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 12
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 164:

Xaa Ala Leu Ala Ala Ala Gly Tyr Asp Val Glu Lys
 1 5 10

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 165:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 5
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in position 1 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 165:

Xaa Leu Val Leu Arg
 1 5

- (2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 166:
- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 11
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS:
 - (D) TOPOLOGY: linear
 - (ix) FEATURE:
 - (D) OTHER INFORMATION: Xaa in positions 1, 2, and 3 is unknown.
 - (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 166:

Xaa Xaa Xaa Tyr Pro Gly Gln Ile Thr Ser Asn
 1 5 10

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 167:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 60
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N in positions 25 and 36 is unknown.

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 167:

ATAGGGAAGG GCGGGGGAAG GGTCNCCCTC NGCAGGGCCG GGCTTGCCTC TGGAGCCTCT

60

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 168:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 18
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (ix) FEATURE:
 (D) OTHER INFORMATION: N in position 16 is unknown.
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 168:

TTTACACATA TATTCNCC 18

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 169:
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 21
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 169:

Glu	Thr	Gln	Pro	Asp	Pro	Gly	Gln	Ile	Leu	Lys	Lys	Val	Pro	Met	Val
1				5					10				15		
Ile	Gly	Ala	Tyr	Thr											
					20										

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 170:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 422
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 170:

Met	Arg	Trp	Arg	Arg	Ala	Pro	Arg	Arg	Ser	Gly	Arg	Pro	Gly	Pro	Arg	
1				5					10					15		
Ala	Gln	Arg	Pro	Gly	Ser	Ala	Ala	Arg	Ser	Ser	Pro	Pro	Leu	Pro	Leu	
			20					25					30			
Leu	Pro	Leu	Leu	Leu	Leu	Leu	Gly	Thr	Ala	Ala	Leu	Ala	Pro	Gly	Ala	
		35					40					45				
Ala	Ala	Gly	Asn	Glu	Ala	Ala	Pro	Ala	Gly	Ala	Ser	Val	Cys	Tyr	Ser	
		50				55					60					
Ser	Pro	Pro	Ser	Val	Gly	Ser	Val	Gln	Glu	Leu	Ala	Gln	Arg	Ala	Ala	
65					70					75					80	
Val	Val	Ile	Glu	Gly	Lys	Val	His	Pro	Gln	Arg	Arg	Gln	Gln	Gly	Ala	
				85					90					95		
Leu	Asp	Arg	Lys	Ala	Ala	Ala	Ala	Ala	Gly	Glu	Ala	Gly	Ala	Trp	Gly	
			100					105					110			
Gly	Asp	Arg	Glu	Pro	Pro	Ala	Ala	Gly	Pro	Arg	Ala	Leu	Gly	Pro	Pro	
		115					120					125				
Ala	Glu	Glu	Pro	Leu	Leu	Ala	Ala	Asn	Gly	Thr	Val	Pro	Ser	Trp	Pro	
		130				135					140					
Thr	Ala	Pro	Val	Pro	Ser	Ala	Gly	Glu	Pro	Gly	Glu	Glu	Ala	Pro	Tyr	
145					150					155					160	
Leu	Val	Lys	Val	His	Gln	Val	Trp	Ala	Val	Lys	Ala	Gly	Gly	Leu	Lys	
				165				170						175		
Lys	Asp	Ser	Leu	Leu	Thr	Val	Arg	Leu	Gly	Thr	Trp	Gly	His	Pro	Ala	
			180					185					190			
Phe	Pro	Ser	Cys	Gly	Arg	Leu	Lys	Glu	Asp	Ser	Arg	Tyr	Ile	Phe	Phe	
		195					200					205				
Met	Glu	Pro	Asp	Ala	Asn	Ser	Thr	Ser	Arg	Ala	Pro	Ala	Ala	Phe	Arg	
		210				215					220					

Ala	Ser	Phe	Pro	Pro	Leu	Glu	Thr	Gly	Arg	Asn	Leu	Lys	Lys	Glu	Val	225	230	235	240
Ser	Arg	Val	Leu	Cys	Lys	Arg	Cys	Ala	Leu	Pro	Pro	Gln	Leu	Lys	Glu	245	250	255	
Met	Lys	Ser	Gln	Glu	Ser	Ala	Ala	Gly	Ser	Lys	Leu	Val	Leu	Arg	Cys	260	265	270	
Glu	Thr	Ser	Ser	Glu	Tyr	Ser	Ser	Leu	Arg	Phe	Lys	Trp	Phe	Lys	Asn	275	280	285	
Gly	Asn	Glu	Leu	Asn	Arg	Lys	Asn	Lys	Pro	Gln	Asn	Ile	Lys	Ile	Gln	290	295	300	
Lys	Lys	Pro	Gly	Lys	Ser	Glu	Leu	Arg	Ile	Asn	Lys	Ala	Ser	Leu	Ala	305	310	315	320
Asp	Ser	Gly	Glu	Tyr	Met	Cys	Lys	Val	Ile	Ser	Lys	Leu	Gly	Asn	Asp	325	330	335	
Ser	Ala	Ser	Ala	Asn	Ile	Thr	Ile	Val	Glu	Ser	Asn	Ala	Thr	Ser	Thr	340	345	350	
Ser	Thr	Thr	Gly	Thr	Ser	His	Leu	Val	Lys	Cys	Ala	Glu	Lys	Glu	Lys	355	360	365	
Thr	Phe	Cys	Val	Asn	Gly	Gly	Glu	Cys	Phe	Met	Val	Lys	Asp	Leu	Ser	370	375	380	
Asn	Pro	Ser	Arg	Tyr	Leu	Cys	Lys	Cys	Pro	Asn	Glu	Phe	Thr	Gly	Asp	385	390	395	400
Arg	Cys	Gln	Asn	Tyr	Val	Met	Ala	Ser	Phe	Tyr	Ser	Thr	Ser	Thr	Pro	405	410	415	
Phe	Leu	Ser	Leu	Pro	Glu											420			

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 171:

Met	Ser	Glu	Arg	Lys	Glu	Gly	Arg	Gly	Lys	Gly	Lys	Gly	Lys	Lys	Lys	1	5	10	15
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	---	---	----	----

Glu Arg Gly Ser Gly Lys Lys Pro Glu Ser Ala Ala Gly Ser Gln Ser
 20 25 30
 Pro Arg Glu Ile Ile Thr Gly Met Pro Ala Ser Thr Glu Gly Ala Tyr
 35 40 45
 Val Ser Ser Glu Ser Pro Ile Arg Ile Ser Val Ser Thr Glu Gly Ala
 50 55 60
 Asn Thr Ser Ser Ser
 65

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 172:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 19
- (B) TYPE: amino acid
- (C) STRANDEDNESS:
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 172:

Arg Lys Gly Asp Val Pro Gly Pro Arg Val Lys Ser Ser Arg Ser Thr
 1 5 10 15

Thr Thr Ala

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 173:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 173:

CGCGAGCGCC	TCAGCGCGGC	CGCTCGCTCT	CCCCCTCGAG	GGACAAACTT	TTCCCAAACC	60
CGATCCGAGC	CCTTGGACCA	AACTCGCCTG	CGCCGAGAGC	CGTCCGCGTA	GAGCGCTCCG	120
TCTCCGGCGA	GATGTCCGAG	CGCAAAGAAG	GCAGAGGCAA	AGGGAAGGGC	AAGAAGAAGG	180
AGCGAGGCTC	CGGCAAGAAG	CCGGAGTCCG	CGGCGGGCAG	CCAGAGCCCA	G	231

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 174:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 178
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 174:

CCTTGCCTCC	CCGATTGAAA	GAGATGAAAA	GCCAGGAATC	GGCTGCAGGT	TCCAAACTAG	60
TCCTTCGGTG	TGAAACCAGT	TCTGAATACT	CCTCTCTCAG	ATTCAAGTGG	TTCAAGAATG	120
GGAATGAATT	GAATCGAAAA	AACAAACCAC	AAAATATCAA	GATACAAAAA	AAGCCAGG	178

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 122
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 175:

GAAGTCAGAA	CTTCGCATTA	ACAAAGCATC	ACTGGCTGAT	TCTGGAGAGT	ATATGTGCAA	60
AGTGATCAGC	AAATTAGGAA	ATGACAGTGC	CTCTGCCAAT	ATCACCATCG	TGGAATCAAA	120
CG						122

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 102
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 176:

AGATCATCAC	TGGTATGCCA	GCCTCAACTG	AAGGAGCATA	TGTGTCTTCA	GAGTCTCCCA	60
TTAGAATATC	AGTATCCACA	GAAGGAGCAA	ATACTTCTTC	AT		102

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 128
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 177:

CTACATCTAC ATCCACCACT GGGACAAGCC ATCTTGTAAG ATGTGCGGAG AAGGAGAAAA	60
CTTTCTGTGT GAATGGAGGG GAGTGCTTCA TGGTGAAAGA CCTTTCAAAC CCCTCGAGAT	120
ACTTGTGC	128

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 178:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 178:

AAGTGCCAAC CTGGATTCAC TGGAGCAAGA TGTACTGAGA ATGTGCCCAT GAAAGTCCAA	60
AACCAAGAA	69

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 179:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 179:

TCGGGCTCCA TGAAGAAGAT GTA	23
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 180

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 23
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 180:

TCCATGAAGA AGATGTACCT GCT	23
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(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 181

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 181:

ATGTACCTGC TGTCTCCTT GA

22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 182

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 22
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 182:

TTGAAGAAGG ACTCGCTGCT CA

22

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 183

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 183:

AAAGCCGGGG GCTTGAAGAA

20

(2) INFORMATION FOR SEQUENCE IDENTIFICATION NUMBER: 184

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 20
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 184:

ATGARGTGTG GGCGGCGAAA

20